

**Population genomics of an endemic Mediterranean fish: differentiation by fine scale  
dispersal and adaptation**

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**Supplementary Table S1: Pairwise genetic distances among locations using outlier and neutral SNPs.**

F <sub>ST</sub>	KAP	VIR	TRE	TOG	OTR	POC
<b>KAP</b>	-	0.0005	<b>0.0116</b>	<b>0.0023</b>	0.0026	<b>0.0032</b>
<b>VIR</b>	<b>0.0257</b>	-	<b>0.0094</b>	<b>0.0021</b>	<b>0.0028</b>	<b>0.0033</b>
<b>TRE</b>	<b>0.3389</b>	<b>0.2749</b>	-	<b>0.0064</b>	<b>0.0064</b>	<b>0.0066</b>
<b>TOG</b>	<b>0.1036</b>	<b>0.0655</b>	<b>0.2475</b>	-	0.0004	0.0003
<b>OTR</b>	<b>0.1704</b>	<b>0.1172</b>	<b>0.1885</b>	<b>0.0906</b>	-	0.0005
<b>POC</b>	<b>0.0952</b>	<b>0.2383</b>	<b>0.2383</b>	-0.0076	<b>0.0875</b>	-

Pairwise genetic distances ( $F_{ST-WC}$ ) among locations of *S. tinca* within the Adriatic Sea, using the 19 outlier SNPs obtained through coalescent and Bayesian simulations (below the diagonal), and the 3,934 neutral SNPs (above the diagonal). Significant values after FDR correction in bold (for a P-value<0.05, FDR=0.0151). KAP: Karaburun Peninsula, Albania; VIR: Island of Vir, Croatia; TRE: Tremiti Islands, Italy; TOG: Torre Guaceto, Italy; OTR: Otranto, Italy and POC: Porto Cesareo, Italy.

Supplementary Table S2: Percentage of assignment of all locations of the 176 individuals of *Syphodus tinca* using all SNPs

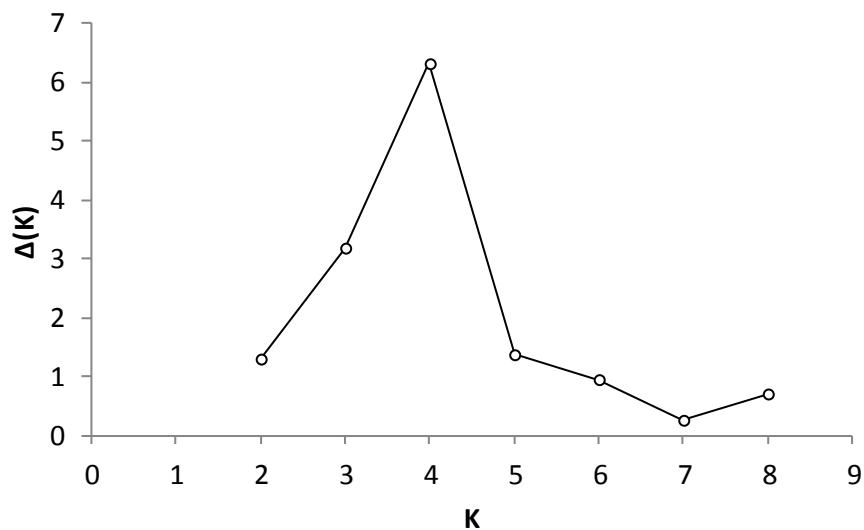
	Locations						Populations				
	KAP	VIR	TRE	TOG	OTR	POC	Unassigned	East	South-west	Tremiti	Unassigned
<b>KAP</b>	<b>28.6</b>	46.4	0.0	14.3	0.0	0.0	10.7	<b>78.6</b>	10.7	0.0	10.7
<b>VIR</b>	20.0	<b>51.4</b>	0.0	14.3	0.0	5.7	8.6	<b>68.6</b>	14.3	0.0	17.1
<b>TRE</b>	0.0	0.0	<b>95.5</b>	4.6	0.0	0.0	0.0	0.0	13.6	<b>68.2</b>	18.2
<b>TOG</b>	3.1	3.1	0.0	<b>46.9</b>	6.3	21.9	18.8	0.0	<b>93.8</b>	0.0	6.3
<b>OTR</b>	0.0	10.3	0.0	20.7	<b>41.4</b>	24.1	3.5	0.0	<b>100.0</b>	0.0	0.0
<b>POC</b>	0.0	3.3	0.0	33.3	0.0	<b>43.3</b>	20.0	0.0	<b>100.0</b>	0.0	0.0

Each cell contains the percentage of individuals sampled in a given location (row) that is assigned to each location or population (columns) according to the Bayesian analysis implemented in GeneClass2. Bold values represent self-assignments. The ‘Unassigned’ columns includes the percentage of individuals with an assignment score lower than 0.95. KAP: Karaburun Peninsula, Albania; VIR: Island of VIR, Croatia; TRE: Tremiti Islands, Italy; TOG: Torre Guaceto, Italy; OTR: Otranto, Italy and POC: Porto Cesareo, Italy. The three populations are defined based on the significance of pairwise comparisons (Fig. 4a) and include East Adriatic (KAP and VIR), South-west Adriatic (TOG, OTR and POC) and Tremiti Islands (TRE).

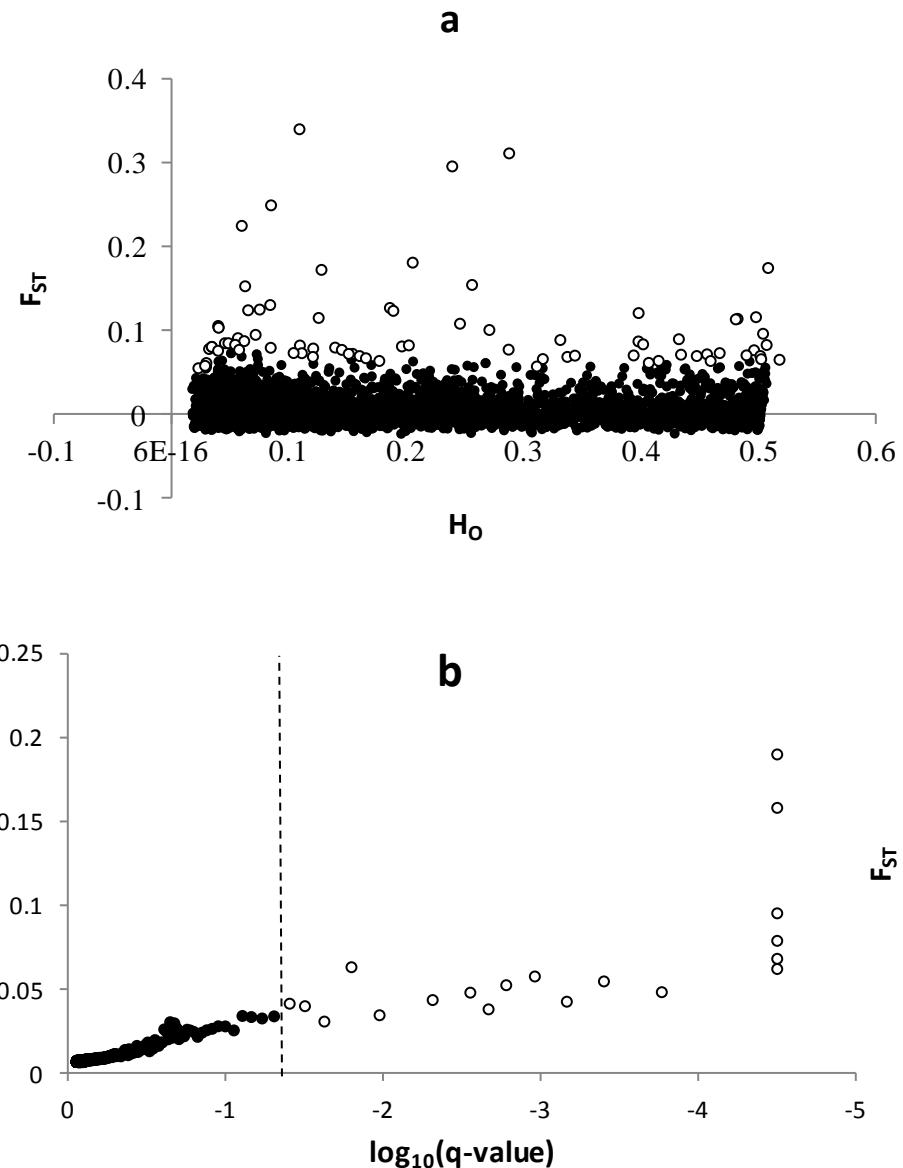
**Supplementary Table S3: Results of the BLASTN analysis of the 12 outlier SNPs under positive selection**

SNP	Gene	Distance (bp)	Length (bp)	E-val	%ID	$F_{ST-WC}$	Function
S1_6614124	ENSONIT00000014653	71,199	64	6.00E-09	81	0.0559 <sup>A</sup>	Uncharacterized protein
S1_6225026	flrt2	106,849	64	1.00E-10	86	0.3115 <sup>A,B</sup>	cell adhesion
S1_5791626	tmem200a	7,868	57	8.00E-07	81	0.1062 <sup>A,B</sup>	integral component of membrane
S1_5429649	pou3f3a	152,163	62	4.00E-14	92	0.1147 <sup>A,B</sup>	transcription, DNA-templated
S1_11289053	CAAP1	32,052	63	3.00E-04	76	0.0844 <sup>A</sup>	apoptotic process
S1_5467344	ddx11	0	46	9.00E-04	83	0.0917 <sup>A</sup>	sister chromatid cohesion
S1_10077133	zranb2	42,075	65	2.00E-09	85	0.0957 <sup>A</sup>	regulation of transcription
S1_2936757	nrp1a	0	50	2.00E-06	84	0.0830 <sup>A</sup>	vascular development
S1_4450333	nbeab	0	49	2.00E-08	90	0.0819 <sup>A</sup>	Uncharacterized protein
S1_2262059	nptx2b	0	64	3.00E-07	78	0.0721 <sup>A</sup>	regulation of circadian rhythm
S1_9653836	ENSONIT00000026164	8,580	64	8.00E-10	83	0.0731 <sup>A</sup>	Uncharacterized protein
S1_10260738	PBX1	3,234	53	4.00E-05	83	0.0767 <sup>A</sup>	transcription factor activity

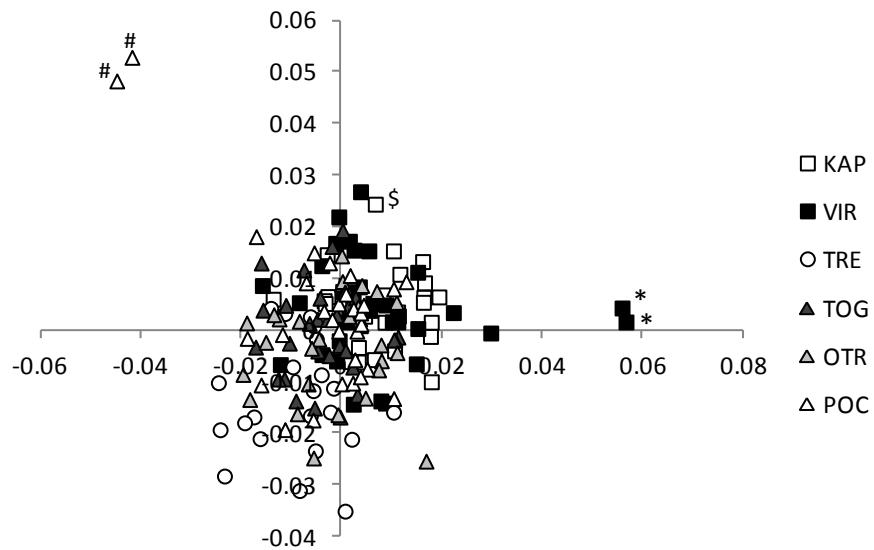
Results with a match against the genome of the Nile tilapia (*Oreochromis niloticus*). For each SNP we provided: the closest gene in the Nile Tilapia genome, the minimum distance between the gene and the SNP (a distance of 0 indicates that the SNP is located within the gene), the length of the alignment, the E-value, the % Identity of the alignment, the overall  $F_{ST-WC}$  among populations for each specific locus and the function according to UniProt. The superscript letters on the  $F_{ST}$  values indicates whether an outlier SNP has been detected by A) ARLEQUIN or B) Bayescan.



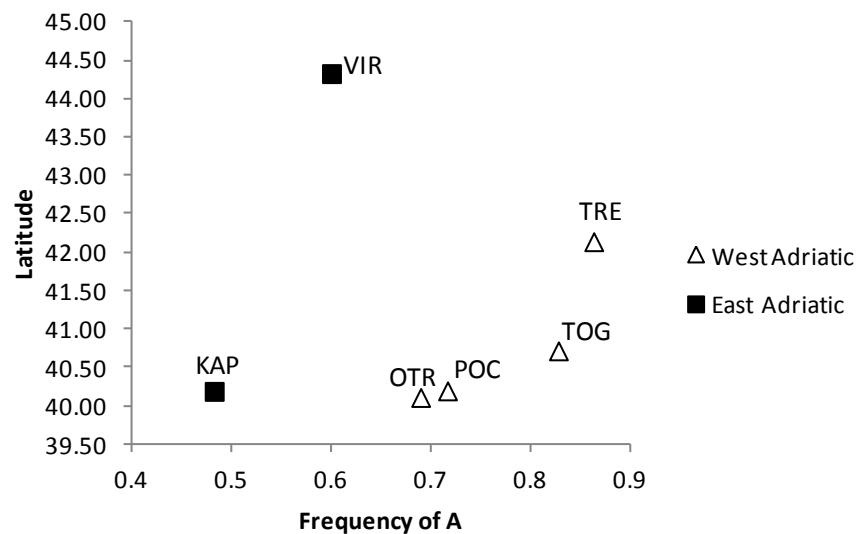
**Supplementary Figure S1:** Detection of the most likely number of genetic groups (K) using STRUCTURE and following the ad hoc statistic  $\Delta(K)$  described in Evanno *et al.* 2005. The most likely number of genetic different groups was K=4.



**Supplementary Figure S2:** Detection of outlier SNPs. a) Using coalescent simulations with ARLEQUIN:  $F_{ST}$ -WC and observed Heterozygosities of all 4,155 SNPs are plotted and significant outlier SNPs shown as open circles (for a P-value<0.05, FDR=0.0054). b) Using bayesian methods with BAYESCAN:  $F_{ST}$ -WC of all 4,155 SNPs are plotted against the  $\log_{10}$  of the q-value. Significant outlier SNPs are shown as open circles. Dashed line represents the cut threshold of 5% of the q-value that delimits the outlier SNPs after FDR.



**Supplementary Figure S3:** MDS analysis of the 176 individuals of *Symphodus tinca* using neutral SNPs and including the divergent individuals from Vir (\*), Porto Cesaeo (#) and Karaburun (\$). KAP: Karaburun Peninsula, Albania; VIR: Island of VIR, Croatia; TRE: Tremiti Islands, Italy; TOG: Torre Guaceto, Italy; OTR: Otranto, Italy and POC: Porto Cesareo, Italy.



**Supplementary Figure S4.** Latitudinal variation of the frequency of the major allele (A) for the SNP S1\_2262059, related to the circadian clock gene (nptx2b) allowing the lariat formation for the correct splicing of Intron 2. KAP: Karaburun Peninsula, Albania; VIR: Island of VIR, Croatia; TRE: Tremiti Islands, Italy; TOG: Torre Guaceto, Italy; OTR: Otranto, Italy and POC: Porto Cesareo, Italy.